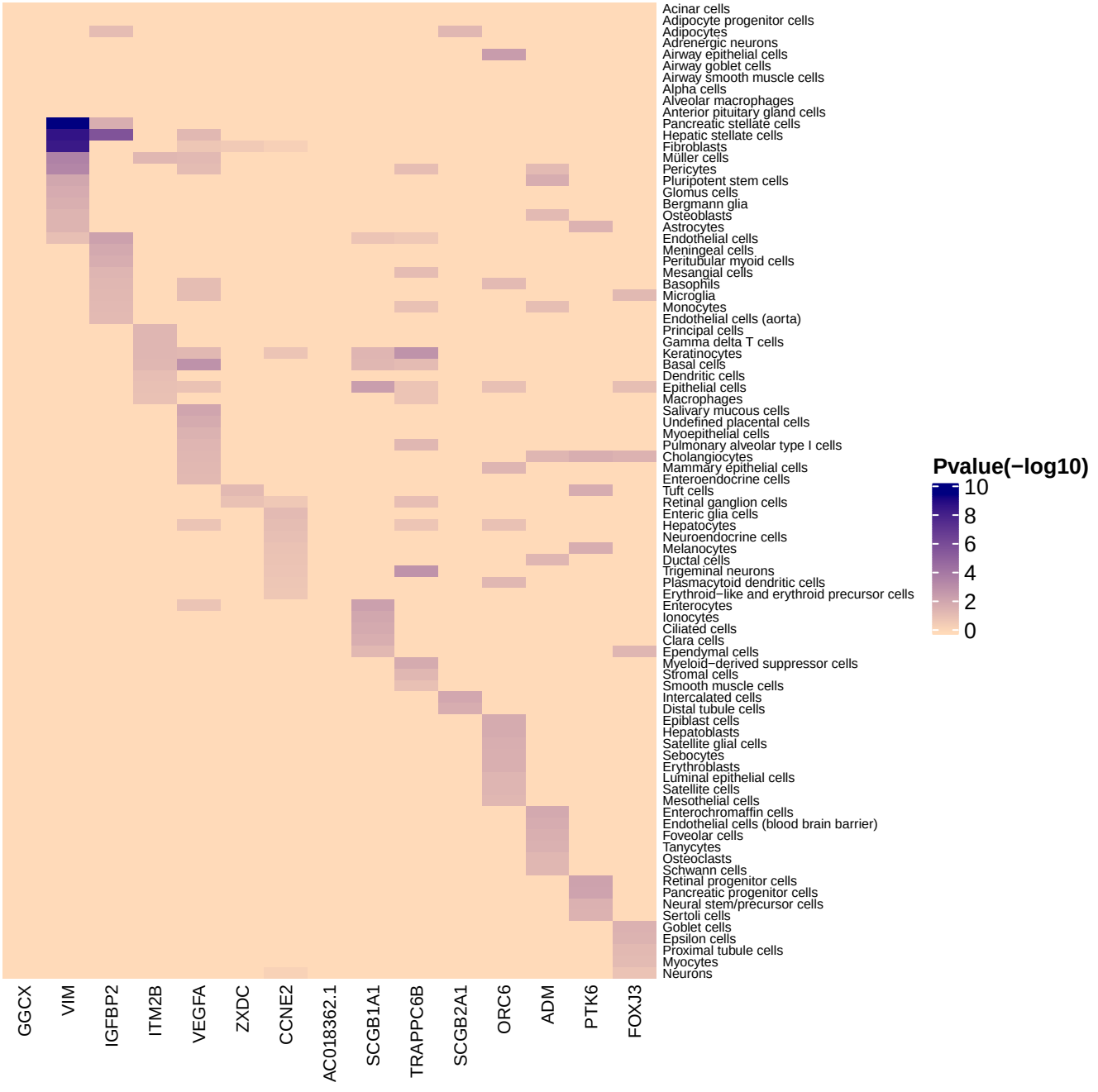
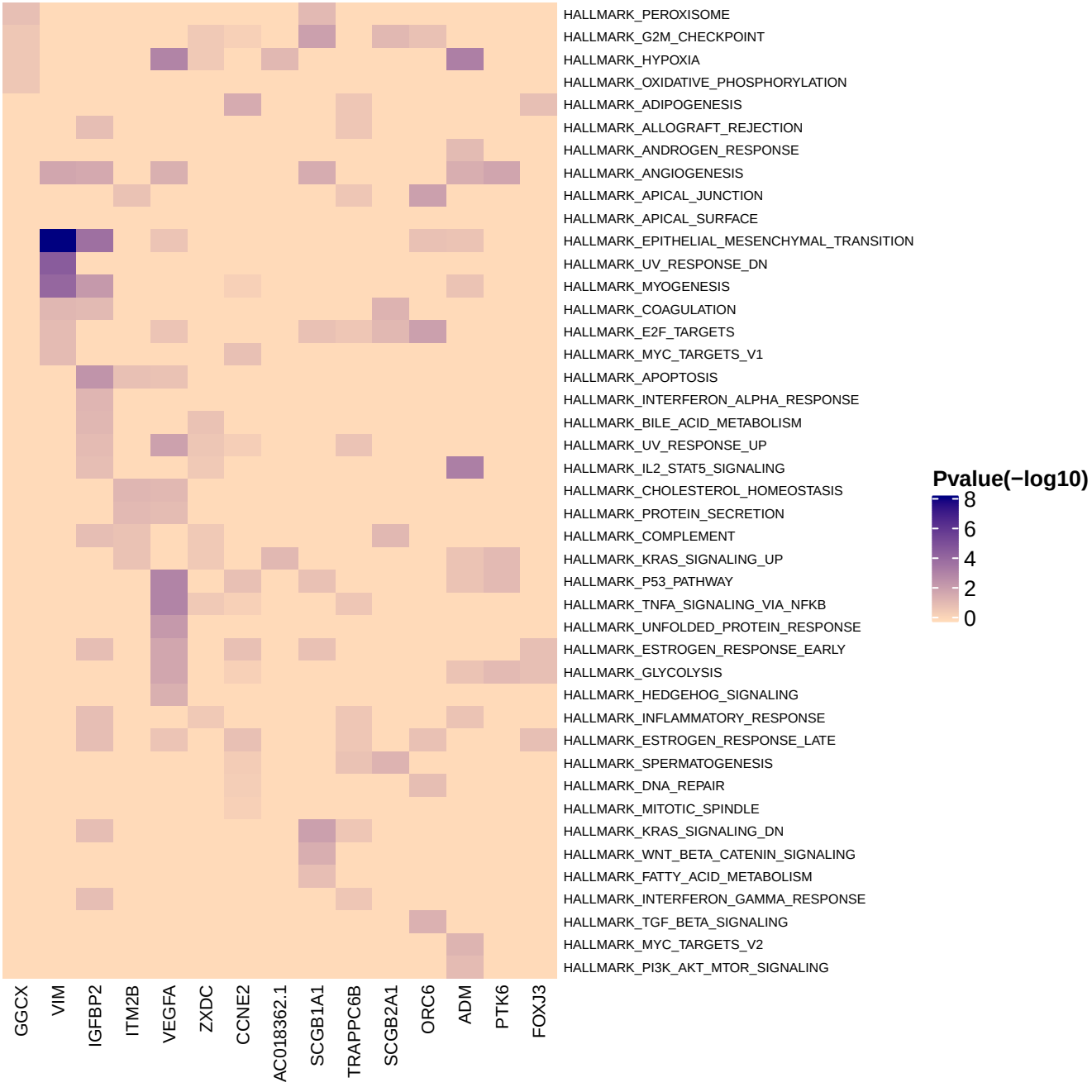
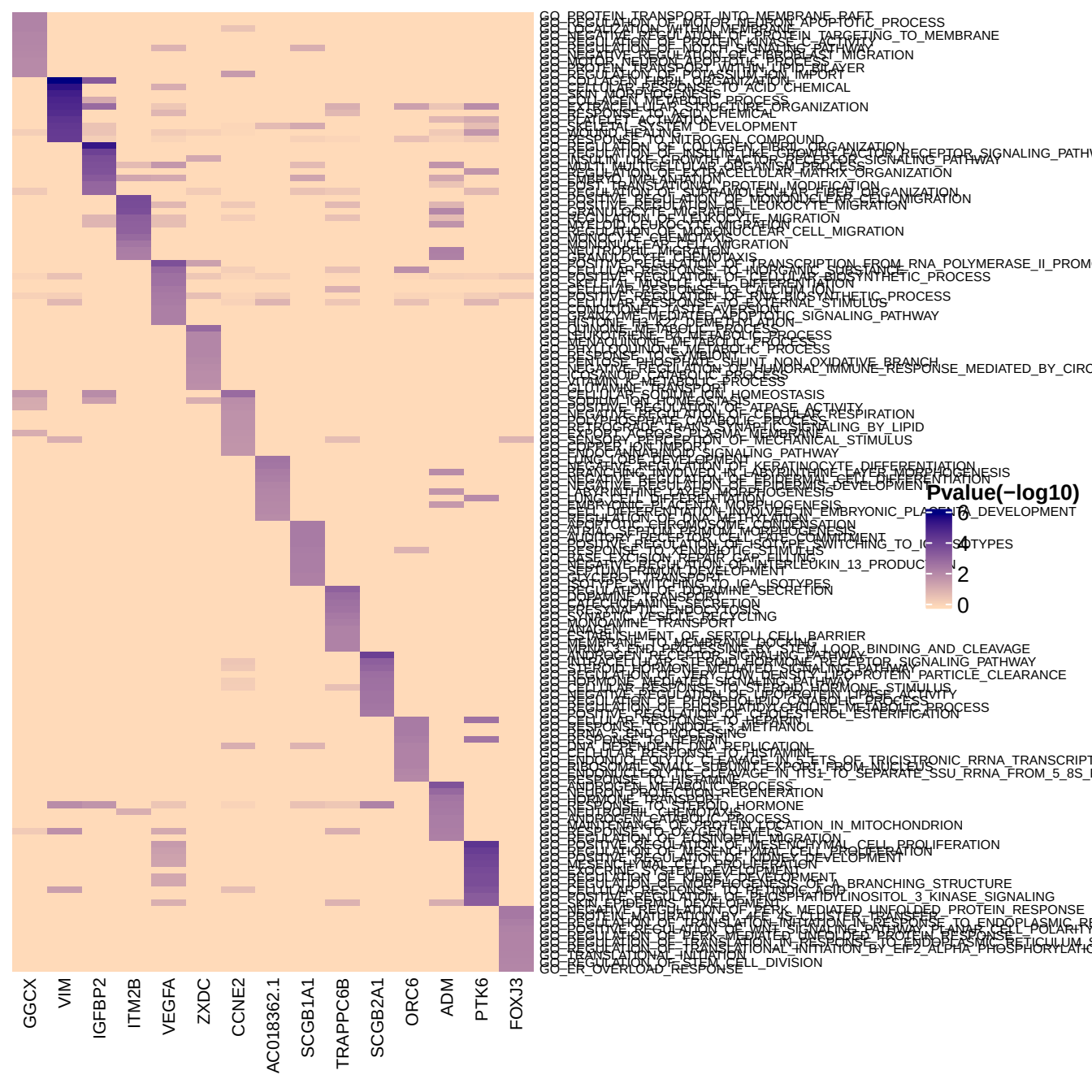
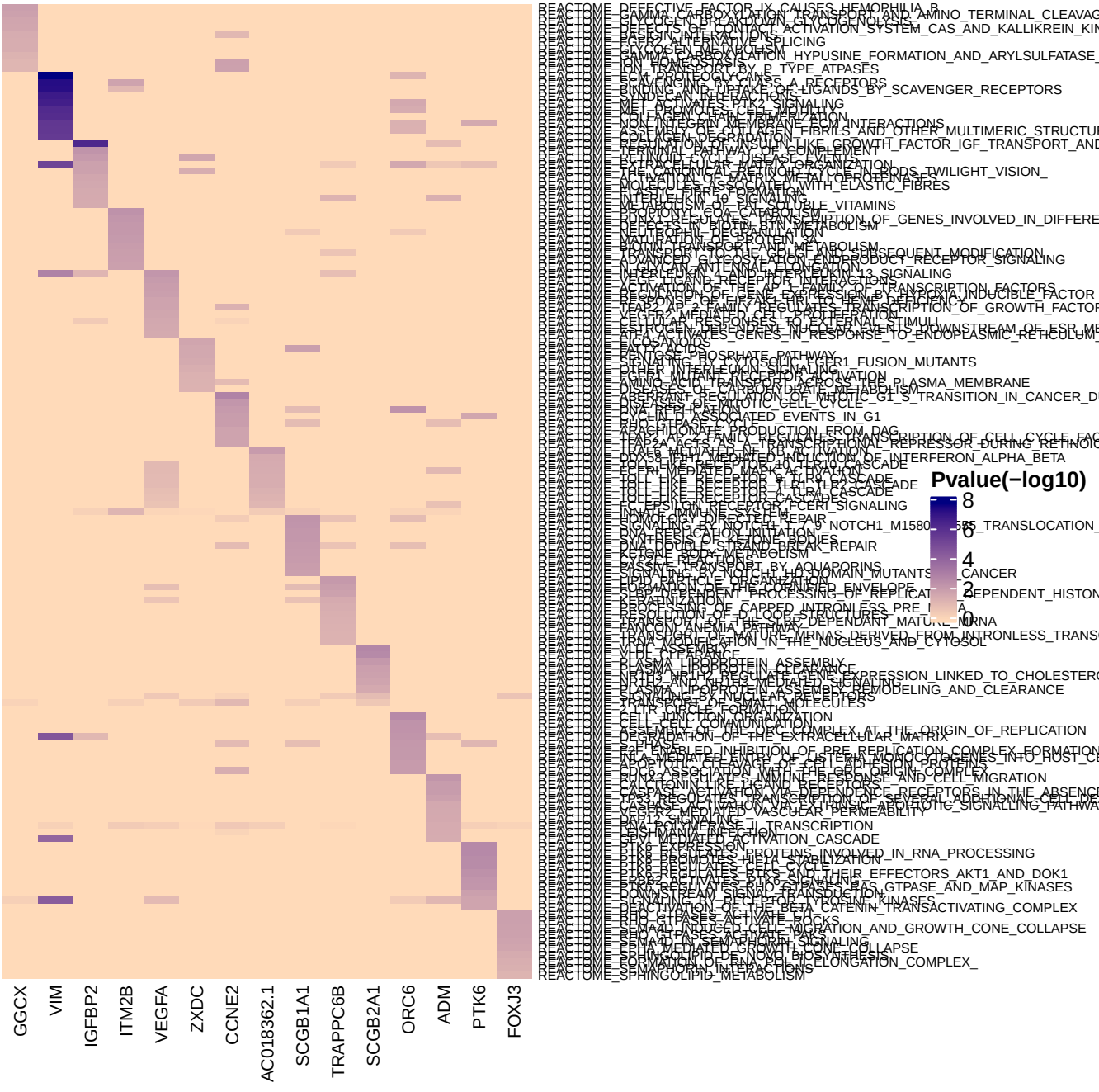

Acinar cells
Adipocyte progenitor cells
Adipocytes
Adrenergic neurons
Airway epithelial cells
Airway goblet cells
Airway smooth muscle cells
Alpha cells
Alveolar macrophages
Anterior pituitary gland cells
Pancreatic stellate cells
Hepatic stellate cells
Fibroblasts
Müller cells
Pericytes
Pluripotent stem cells
Glomus cells
Bergmann glia
Osteoblasts
Astrocytes
Endothelial cells
Meningeal cells
Peritubular myoid cells
Mesangial cells
Basophils
Microglia
Monocytes
Endothelial cells (aorta)
Principal cells
Gamma delta T cells
Keratinocytes
Basal cells
Dendritic cells
Epithelial cells
Macrophages
Salivary mucous cells
Undefined placental cells
Myoepithelial cells
Pulmonary alveolar type I cells
Cholangiocytes
Mammary epithelial cells
Enteroendocrine cells
Tuft cells
Retinal ganglion cells
Enteric glia cells
Hepatocytes
Neuroendocrine cells
Melanocytes
Ductal cells
Trigeminal neurons
Plasmacytoid dendritic cells
Erythroid−like and erythroid precursor cells
Enterocytes
Ionocytes
Ciliated cells
Clara cells
Ependymal cells
Myeloid−derived suppressor cells
Stromal cells
Smooth muscle cells
Intercalated cells
Distal tubule cells
Epiblast cells
Hepatoblasts
Satellite glial cells
Sebocytes
Erythroblasts
Luminal epithelial cells
Satellite cells
Mesothelial cells
Enterochromaffin cells
Endothelial cells (blood brain barrier)
Foveolar cells
Tanycytes
Osteoclasts
Schwann cells
Retinal progenitor cells
Pancreatic progenitor cells
Neural stem/precursor cells
Sertoli cells
Goblet cells
Epsilon cells
Proximal tubule cells
Myocytes
Neurons
GGCX
VIM
IGFBP2
ITM2B
VEGFA
ZXDC
CCNE2
AC018362.1
SCGB1A1
TRAPPC6B
SCGB2A1
ORC6
ADM
PTK6
FOXJ3
Pvalue(−log10)
10
8
6
4
2
0


HALLMARK_PEROXISOME
HALLMARK_G2M_CHECKPOINT
HALLMARK_HYPOXIA
HALLMARK_OXIDATIVE_PHOSPHORYLATION
HALLMARK_ADIPOGENESIS
HALLMARK_ALLOGRAFT_REJECTION
HALLMARK_ANDROGEN_RESPONSE
HALLMARK_ANGIOGENESIS
HALLMARK_APICAL_JUNCTION
HALLMARK_APICAL_SURFACE
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
HALLMARK_UV_RESPONSE_DN
HALLMARK_MYOGENESIS
HALLMARK_COAGULATION
HALLMARK_E2F_TARGETS
HALLMARK_MYC_TARGETS_V1
HALLMARK_APOPTOSIS
HALLMARK_INTERFERON_ALPHA_RESPONSE
HALLMARK_BILE_ACID_METABOLISM
HALLMARK_UV_RESPONSE_UP
HALLMARK_IL2_STAT5_SIGNALING
HALLMARK_CHOLESTEROL_HOMEOSTASIS
HALLMARK_PROTEIN_SECRETION
HALLMARK_COMPLEMENT
HALLMARK_KRAS_SIGNALING_UP
HALLMARK_P53_PATHWAY
HALLMARK_TNFA_SIGNALING_VIA_NFKB
HALLMARK_UNFOLDED_PROTEIN_RESPONSE
HALLMARK_ESTROGEN_RESPONSE_EARLY
HALLMARK_GLYCOLYSIS
HALLMARK_HEDGEHOG_SIGNALING
HALLMARK_INFLAMMATORY_RESPONSE
HALLMARK_ESTROGEN_RESPONSE_LATE
HALLMARK_SPERMATOGENESIS
HALLMARK_DNA_REPAIR
HALLMARK_MITOTIC_SPINDLE
HALLMARK_KRAS_SIGNALING_DN
HALLMARK_WNT_BETA_CATENIN_SIGNALING
HALLMARK_FATTY_ACID_METABOLISM
HALLMARK_INTERFERON_GAMMA_RESPONSE
HALLMARK_TGF_BETA_SIGNALING
HALLMARK_MYC_TARGETS_V2
HALLMARK_PI3K_AKT_MTOR_SIGNALING
GGCX
VIM
IGFBP2
ITM2B
VEGFA
ZXDC
CCNE2
AC018362.1
SCGB1A1
TRAPPC6B
SCGB2A1
ORC6
ADM
PTK6
FOXJ3
Pvalue(−log10)
8
6
4
2
0


GO_PROTEIN_TRANSPORT_INTO_MEMBRANE_RAFT
GO_LOCALIZATION_WITHIN_MEMBRANE
GO_NEGATIVE_REGULATION_OF_APOPTOTIC_PROCESS
GO_NEGATIVE_REGULATION_OF_PROTEIN_TARGETING_TO_MEMBRANE
GO_REGULATION_OF_NOTCH_SIGNALING_PATHWAY
GO_NEGATIVE_REGULATION_OF_FIBROBLAST_MIGRATION
GO_MOTOR_NEURON_APOPTOTIC_PROCESS
GO_PROTEIN_TRANSPORT_WITHIN_LIPID_BILAYER
GO_REGULATION_OF_POTASSIUM_ION_IMPORT
GO_COLLAGEN_FIBRIL_ORGANIZATION
GO_CELLULAR_RESPONSE_TO_FATTY_ACID_CHEMICAL
GO_SKIN_MORPHOGENESIS
GO_COLLAGEN_METABOLIC_PROCESS
GO_EXTRACELLULAR_STRUCTURE_ORGANIZATION
GO_RESPONSE_TO_FATTY_ACID_CHEMICAL
GO_PLATELET_ACTIVATION
GO_CLATHRIN_COAT_ASSEMBLY
GO_WOUND_HEALING
GO_EMBRYONIC_DEVELOPMENT
GO_RESPONSE_TO_NITROGEN_COMPOUND
GO_REGULATION_OF_CELL_CELL_ADHESION
GO_REGULATION_OF_INSULIN-LIKE_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHW
GO_INSULIN-LIKE_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY
GO_MULTICELLULAR_ORGANISM_METABOLISM
GO_REGULATION_OF_EXTRACELLULAR_MATRIX_ORGANIZATION
GO_FIBRIN_IMPLANTATION
GO_POST-TRANSLATIONAL_PROTEIN_MODIFICATION
GO_REGULATION_OF_SUPPRAMOLECULAR_FIBER_ORGANIZATION
GO_POSITIVE_REGULATION_OF_MONONUCLEAR_CELL_MIGRATION
GO_LEUKOCYTE_MIGRATION
GO_GRANULOCYTE_MIGRATION
GO_REGULATION_OF_LEUKOCYTE_MIGRATION
GO_MYELOID_LEUKOCYTE_MIGRATION
GO_REGULATION_OF_MONONUCLEAR_CELL_MIGRATION
GO_MONOCYTE_CHEMOTAXIS
GO_MONONUCLEAR_CELL_MIGRATION
GO_NEUTROPHIL_MIGRATION
GO_NEUTROPHIL_CHEMOTAXIS
GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROM
GO_CELLULAR_RESPONSE_TO_LIPOPOLYSACCHARIDE
GO_POSITIVE_REGULATION_OF_CELLULAR_BIOSYNTHETIC_PROCESS
GO_POSITIVE_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION
GO_CELLULAR_RESPONSE_TO_CALCIUM_ION
GO_POSITIVE_REGULATION_OF_BIOSYNTHETIC_PROCESS
GO_CELLULAR_RESPONSE_TO_EXTERNAL_STIMULUS
GO_CONDITIONED_TASTE_AVERSION
GO_WNT_MEDIATED_ACTIVATION_OF_DVL_ACTIVITY_SIGNALING_PATHWAY
GO_HISTONE_H3-K27_DEMETHYLATION
GO_NUCLEOTIDE_METABOLIC_PROCESS
GO_QUINONE_METABOLIC_PROCESS
GO_MENAQUINONE_METABOLIC_PROCESS
GO_PHYLLOQUINONE_METABOLIC_PROCESS
GO_RESPONSE_TO_ANTIBIOTIC
GO_PENTOSE_PHOSPHATE_SHUNT_NON_OXIDATIVE_BRANCH
GO_NEGATIVE_REGULATION_OF_HUMORAL_IMMUNE_RESPONSE_MEDIATED_BY_CIRC
GO_FOLIC_ACID_METABOLIC_PROCESS
GO_VITAMIN_METABOLIC_PROCESS
GO_CELLULAR_ZINC_ION_HOMEOSTASIS
GO_CELLULAR_SODIUM_ION_HOMEOSTASIS
GO_SODIUM_ION_HOMEOSTASIS
GO_POSITIVE_REGULATION_OF_ATPASE_ACTIVITY
GO_NEGATIVE_REGULATION_OF_CELLULAR_RESPIRATION
GO_PHOSPHOLIPID_BIOSYNTHETIC_PROCESS
GO_RETROGRADE_TRANSLOCATION_PROCESS
GO_RETROGRADE_TRANS-SYNAPTIC_SIGNALING_BY_LIPID
GO_SENSORY_PERCEPTION_OF_MECHANICAL_STIMULUS
GO_COPPER_ION_IMPORT
GO_CANONICAL_WNT_SIGNALING_PATHWAY
GO_LUNG_TUBE_DEVELOPMENT
GO_NEGATIVE_REGULATION_OF_KERATINOCYTE_DIFFERENTIATION
GO_BRANCHING_INVOLVED_IN_LABYRINTHINE_LAYER_MORPHOGENESIS
GO_NEGATIVE_REGULATION_OF_EPIDERMAL_CELL_DIFFERENTIATION
GO_NEGATIVE_REGULATION_OF_EPIDERMIS_DEVELOPMENT
GO_LABYRINTHINE_LAYER_MORPHOGENESIS
GO_T_CELL_DIFFERENTIATION
GO_EMBRYONIC_PLACENTA_MORPHOGENESIS
GO_CELL_DIFFERENTIATION_INVOLVED_IN_EMBRYONIC_PLACENTA_DEVELOPMENT
GO_REGULATION_OF_DNA_METHYLATION
GO_APOPTOTIC_CHROMOSOME_CONDENSATION
GO_AORTA_SEPTUM_MORPHOGENESIS
GO_AUDITORY_RECEPTOR_CELL_FATE_COMMITMENT
GO_NEGATIVE_REGULATION_OF_ISOTYPE_SWITCHING_TO_IGG_ISOTYPES
GO_RESPONSE_TO_XENOBIOTIC_STIMULUS
GO_NUCLEOTIDE_EXCISION_REPAIR_GAP_FILLING
GO_NEGATIVE_REGULATION_OF_GAMMA_INTERLEUKIN_13_PRODUCTION
GO_SEPTUM_PRIMUM_DEVELOPMENT
GO_ERYTHROCYTE_TRANSPORT
GO_ISOTYPE_SWITCHING_TO_IGA_ISOTYPES
GO_REGULATION_OF_DOPAMINE_SECRETION
GO_DOPAMINE_TRANSPORT
GO_CATECHOLAMINE_SECRETION
GO_ADRENALIN_SECRETION
GO_FORMAL_DEHYDROGENASE_CYCLING
GO_MONOAMINE_TRANSPORT
GO_ESTABLISHMENT_OF_SERTOLI_CELL_BARRIER
GO_MEMBRANE_TO_MEMBRANE_DOCKING
GO_MEMBRANE_END_DOCKING_SNARE_BINDING_AND_CLEAVAGE
GO_NUCLEOCYTOPLASMIC_TRANSPORTING_RECEPTOR_BINDING_AND_CLEAVAGE
GO_INTRACELLULAR_STEROID_HORMONE_RECEPTOR_SIGNALING_PATHWAY
GO_REGULATION_OF_VERY_LOW_DENSITY_LIPOPROTEIN_PARTICLE_CLEARANCE
GO_REGULATION_OF_VERY_LOW_DENSITY_LIPOPROTEIN_PARTICLE_CLEARANCE
GO_CELLULAR_RESPONSE_TO_STEROID_HORMONE_STIMULUS
GO_NEGATIVE_REGULATION_OF_PHOSPHOLIPASE_ACTIVITY
GO_NEGATIVE_REGULATION_OF_PHOSPHOLIPID_BIOSYNTHETIC_PROCESS
GO_REGULATION_OF_PHOSPHATIDYLCHOLINE_METABOLIC_PROCESS
GO_POSITIVE_REGULATION_OF_CHOLESTEROL_ESTERIFICATION
GO_CELLULAR_RESPONSE_TO_HEPARIN
GO_RESPONSE_TO_INDOLE-3-METHANOL
GO_RNA_3'-END_PROCESSING
GO_RNA_PROCESSING_HEPARIN
GO_DNA_DEPENDENT_DNA_REPLICATION
GO_CELLULAR_RESPONSE_TO_HISTAMINE
GO_ENDONUCLEOLYTIC_CLEAVAGE_TO_GENERATE_TARGETS_OF_TRICISTRONIC_RRNA_TRANSCRIPT
GO_RIBOSOMAL_SMALL_SUBUNIT_EXPORT_FROM_NUCLEUS
GO_CONSTITUTIVE_SITE_CLEAVAGE_IN_ITS1_TO_SEPARATE_SSU_RRNA_FROM_5_8S_
GO_RESPONSE_TO_HISTAMINE
GO_ANDROGEN_METABOLIC_PROCESS
GO_ANDROGEN_BIOSYNTHETIC_PROCESS
GO_TISSUE_PROGENITOR_REGENERATION
GO_HORMONE_TRANSPORT
GO_RESPONSE_TO_STEROID_HORMONE
GO_NEUTROPHIL_CHEMOTAXIS
GO_NITROGEN_CATABOLIC_PROCESS
GO_MAINTENANCE_OF_PROTEIN_LOCATION_IN_MITOCHONDRION
GO_RESPONSE_TO_OXYGEN_LEVEL
GO_REGULATION_OF_EOSINOPHIL_MIGRATION
GO_POSITIVE_REGULATION_OF_MESENCHYMAL_CELL_PROLIFERATION
GO_POSITIVE_REGULATION_OF_MESENCHYMAL_CELL_PROLIFERATION
GO_POSITIVE_REGULATION_OF_KIDNEY_DEVELOPMENT
GO_MESENCHYMAL_CELL_PROLIFERATION
GO_EPITHELIAL_TUBE_MORPHOGENESIS
GO_REGULATION_OF_KIDNEY_DEVELOPMENT
GO_REGULATION_OF_MORPHOGENESIS_OF_A_BRANCHING_STRUCTURE
GO_CELLULAR_RESPONSE_TO_RETINOIC_ACID
GO_PHOSPHATIDYLINOSITOL_3_KINASE_SIGNALING
GO_SKIN_EPIDERMIS_DEVELOPMENT
GO_NEGATIVE_REGULATION_OF_PERK_MEDIATED_UNFOLDED_PROTEIN_RESPONSE
GO_PROTEIN_MATURATION_BY_PEPTIDYL_PROLYL_TRANS/CIS_ISOMERASE_ACTIVITY
GO_NEGATIVE_REGULATION_OF_TRANSLATION_INITIATION_IN_RESPONSE_TO_ENDOPLASMIC_RE
GO_POSITIVE_REGULATION_OF_WNT_SIGNALING_PATHWAY_PLANAR_CELL_POLARITY
GO_REGULATION_OF_PERK_MEDIATED_UNFOLDED_PROTEIN_RESPONSE
GO_REGULATION_OF_TRANSLATION_INITIATION_IN_RESPONSE_TO_ENDOPLASMIC_RETICULUM_S
GO_REGULATION_OF_TRANSLATIONAL_INITIATION_BY_EIF2_ALPHA_PHOSPHORYLATIO
GO_TRANSLATIONAL_INITIATION
GO_REGULATION_OF_INTRA_S_PHASE_CELL_DIVISION
GO_ER_OVERLOAD_RESPONSE
GGCX
VIM
IGFBP2
ITM2B
VEGFA
ZXDC
CCNE2
AC018362.1
SCGB1A1
TRAPPC6B
SCGB2A1
ORC6
ADM
PTK6
FOXJ3
Pvalue(−log10)
6
4
2
0

KEGG_PROXIMAL_TUBULE_BICARBONATE_RECLAMATION
KEGG_ALDOSTERONE_REGULATED_SODIUM_REABSORPTION
KEGG_CARDIAC_MUSCLE_CONTRACTION
KEGG_SPLICEOSOME
KEGG_INSULIN_SIGNALING_PATHWAY
KEGG_CALCIUM_SIGNALING_PATHWAY
KEGG_MAPK_SIGNALING_PATHWAY
KEGG_ABC_TRANSPORTERS
KEGG_ACUTE_MYELOID_LEUKEMIA
KEGG_ADHERENS_JUNCTION
KEGG_ECM_RECEPTOR_INTERACTION
KEGG_FOCAL_ADHESION
KEGG_ADIPOCYTOKINE_SIGNALING_PATHWAY
KEGG_ALANINE_ASPARTATE_AND_GLUTAMATE_METABOLISM
KEGG_ALLOGRAFT_REJECTION
KEGG_ALPHA_LINOLENIC_ACID_METABOLISM
KEGG_PRION_DISEASES
KEGG_COMPLEMENT_AND_COAGULATION_CASCADES
KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS
KEGG_PROPANOATE_METABOLISM
KEGG_PORPHYRIN_AND_CHLOROPHYLL_METABOLISM
KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION
KEGG_N_GLYCAN_BIOSYNTHESIS
KEGG_VIBRIO_CHOLERAE_INFECTION
KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION
KEGG_LYSOSOME
KEGG_CELL_ADHESION_MOLECULES_CAMS
KEGG_BLADDER_CANCER
KEGG_PATHWAYS_IN_CANCER
KEGG_MTOR_SIGNALING_PATHWAY
KEGG_COLORECTAL_CANCER
KEGG_PANCREATIC_CANCER
KEGG_RENAL_CELL_CARCINOMA
KEGG_LEISHMANIA_INFECTION
KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY
KEGG_VEGF_SIGNALING_PATHWAY
KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY
KEGG_PENTOSE_PHOSPHATE_PATHWAY
KEGG_P53_SIGNALING_PATHWAY
KEGG_SMALL_CELL_LUNG_CANCER
KEGG_PROSTATE_CANCER
KEGG_CELL_CYCLE
KEGG_MISMATCH_REPAIR
KEGG_PRIMARY_IMMUNODEFICIENCY
KEGG_DNA_REPLICATION
KEGG_RIG_I_LIKE_RECEPTOR_SIGNALING_PATHWAY
KEGG_GNRH_SIGNALING_PATHWAY
KEGG_NEUROTROPHIN_SIGNALING_PATHWAY
KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS
KEGG_BUTANOATE_METABOLISM
KEGG_BASE_EXCISION_REPAIR
KEGG_LYSINE_DEGRADATION
KEGG_NUCLEOTIDE_EXCISION_REPAIR
KEGG_NOTCH_SIGNALING_PATHWAY
KEGG_PPAR_SIGNALING_PATHWAY
KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450
KEGG_PYRIMIDINE_METABOLISM
KEGG_PURINE_METABOLISM
KEGG_HOMOLOGOUS_RECOMBINATION
KEGG_VIRAL_MYOCARDITIS
KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY
KEGG_ALZHEIMERS_DISEASE
KEGG_AMINO_SUGAR_AND_NUCLEOTIDE_SUGAR_METABOLISM
KEGG_HISTIDINE_METABOLISM
KEGG_THYROID_CANCER
KEGG_O_GLYCAN_BIOSYNTHESIS
KEGG_TRYPTOPHAN_METABOLISM
KEGG_GALACTOSE_METABOLISM
KEGG_FRUCTOSE_AND_MANNOSE_METABOLISM
KEGG_TYPE_II_DIABETES_MELLITUS
KEGG_STARCH_AND_SUCROSE_METABOLISM
KEGG_GLYCOLYSIS_GLUCONEOGENESIS
KEGG_FC_EPSILON_RI_SIGNALING_PATHWAY
KEGG_GLIOMA
KEGG_MELANOMA
KEGG_GAP_JUNCTION
KEGG_REGULATION_OF_ACTIN_CYTOSKELETON
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION
KEGG_TIGHT_JUNCTION
GGCX
VIM
IGFBP2
ITM2B
VEGFA
ZXDC
CCNE2
AC018362.1
SCGB1A1
TRAPPC6B
SCGB2A1
ORC6
ADM
PTK6
FOXJ3
Pvalue(−log10)
6
4
2
0


Pvalue(−log10)
8
6
4
2
0
GGCX
VIM
IGFBP2
ITM2B
VEGFA
ZXDC
CCNE2
AC018362.1
SCGB1A1
TRAPPC6B
SCGB2A1
ORC6
ADM
PTK6
FOXJ3
REACTOME_DEFECTIVE_FACTOR_IX_CAUSES_HEMOPHILIA_B
REACTOME_GLYCOGEN_BREAKDOWN_(GLYCOGENOLYSIS)
REACTOME_DEFECTS_OF_CONTACT_ACTIVATION_SYSTEM_CAS_AND_KALLIKREIN_KIN
REACTOME_PASSIVE_TRANSPORT_BY_AQUAPORINS
REACTOME_SIGNALING_BY_NOTCH1_HD_DOMAIN_MUTANTS_CANCER
REACTOME_ASSEMBLY_OF_THE_ORC_COMPLEX_AT_THE_ORIGIN_OF_REPLICATION
REACTOME_CELL_CELL_COMMUNICATION
REACTOME_DEGRADATION_OF_THE_EXTRACELLULAR_MATRIX
REACTOME_RHO_GTPASES_ACTIVATE_ROCKS
REACTOME_SPHINGOLIPID_METABOLISM